

Scoring table: BLOSUM62							Alignments						
Searched: 1612378 seqs, 512079187 residues							Total number of hits satisfying chosen parameters: 1612378						
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries							Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
Result No.	Score	Query	Match	Length	DB	ID	Description						
1	4081	100.0	766	2	Q76B58		076B58 homo sapien	Query Match	100.0%	Score 4081;	DB 2;	Length 766;	
2	4081	98.2	766	2	Q8K0R9		Q8K0R9 mus musculu	Best Local Similarity	100.0%	Pred. No. 2.	2e-285;		
3	3998	98.0	766	2	Q8K1M7		Q8K1M7 rattus norv	Matches 766;	Conservative	0;	Mismatches 0;	Indels 0;	
4	2968	72.7	783	2	Q6DFY8		Q6DFY8 mus musculu						
5	2963	72.5	788	2	Q8T96		Q8T96 mus musculu	QY	1	MINWRAGAEGLFSIMALNEWIAISLHCWLVAVAVSDOHA	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	60	
6	2962	72.6	781	2	Q95560		Q95560 homo sapien	DB	1	MINWRAGAEGLFSIMALNEWIAISLHCWLVAVAVSDOHA	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	60	
7	2962	72.6	783	2	Q8N360		Q8N360 homo sapien						
8	2962	72.6	783	2	Q8K1M8		Q8K1M8 rattus norv	QY	61	TDFVDRSGESTRYKILPRAEFTPNIRLLGRPTL	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	120	
9	2962	72.6	791	2	Q9C0B6		Q9C0B6 homo sapien	DB	61	TDFVDRSGESTRYKILPRAEFTPNIRLLGRPTL	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	120	
10	2474.5	60.6	678	2	Q6ZWC1		Q6ZWC1 homo sapien						
11	2184	53.5	761	2	Q7ZRZ3		Q7ZRZ3 gallus galli	QY	121	QTQENLKKYGHFLSATLGEBESLTFDGRKLISRAEGSDSTTNSSSVTLETLLQL	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	180	
12	2161	53.0	761	2	Q6477		Q6477 homo sapien	DB	121	QTQENLKKYGHFLSATLGEBESLTFDGRKLISRAEGSDSTTNSSSVTLETLLQL	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	180	
13	2161	53.0	761	2	Q6P1AO		Q6P1AO homo sapien						
14	2151.5	52.8	760	2	Q92D93		Q92D93 m bmp/retin	QY	121	QTQENLKKYGHFLSATLGEBESLTFDGRKLISRAEGSDSTTNSSSVTLETLLQL	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	180	
15	2151.5	52.7	760	2	Q8C1C9		Q8C1C9 mus musculu	DB	121	QTQENLKKYGHFLSATLGEBESLTFDGRKLISRAEGSDSTTNSSSVTLETLLQL	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	180	
16	2136.5	52.4	760	2	Q92ST8		Q92ST8 rattus norv						
17	2128	52.1	761	2	Q9XL0		Q9XL0 mus musculu	QY	181	AASYFIDRSITLRLHIIQASTAIKVTETRTRGPKFEPNCNCPSNDIQAME	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	240	
18	1434.5	35.5	532	2	Q6LG0		Q6LG0 homo sapien	DB	181	AASYFIDRSITLRLHIIQASTAIKVTETRTRGPKFEPNCNCPSNDIQAME	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	240	
19	1224.5	30.0	476	2	Q6IPV6		Q6IPV6 homo sapien						
20	1142	28.0	218	2	Q95726		Q95726 homo sapien	QY	241	QGLQVLLDDYQLEPVEQALSYTAACNSSEGEFICKENDWCHCCKGPKEPNCNCPSNDIQAME	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	300	
21	1026	25.1	378	2	Q812F0		Q812F0 mus musculu	DB	241	QGLQVLLDDYQLEPVEQALSYTAACNSSEGEFICKENDWCHCCKGPKEPNCNCPSNDIQAME	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	300	
22	970.5	23.8	320	2	Q8WU22		Q8WU22 homo sapien						
23	967.5	23.7	320	2	Q8OZL2		Q8OZL2 mus musculu	QY	301	ENLRITETWKAISDFBBSDBFKLFLMRKLPNNYFLNTSTIMHLWTMSNFQRYYEQLEN	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	360	
24	901	22.1	206	2	Q7LCZ9		Q7LCZ9 homo sapien	DB	301	ENLRITETWKAISDFBBSDBFKLFLMRKLPNNYFLNTSTIMHLWTMSNFQRYYEQLEN	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	360	
25	720.5	17.7	228	2	Q8WX56		Q8WX56 homo sapien						
26	717	4.3	72	2	Q7Q20P4		Q7Q20P4 mus musculu	QY	301	ENLRITETWKAISDFBBSDBFKLFLMRKLPNNYFLNTSTIMHLWTMSNFQRYYEQLEN	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	360	
27	153	3.7	587	1	C08B_0NCMY		C08B_0NCMY oncophryne	DB	361	SMKOLFLRAQKIVHKLFSLSKRCHKQPLISLPRQRTSTYWLTRIQSFLYCNGNLGSFS	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	420	
28	141.5	3.5	1460	2	Q6RHL9		Q6RHL9 mycoplasma						
29	135.5	3.3	684	1	YMW5_YEAST		YMW5_YEAST saccharomyces	QY	361	SMKOLFLRAQKIVHKLFSLSKRCHKQPLISLPRQRTSTYWLTRIQSFLYCNGNLGSFS	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	420	
30	134.5	3.3	799	2	Q6B1N0		Q6B1N0 debaryomyces	DB	361	SMKOLFLRAQKIVHKLFSLSKRCHKQPLISLPRQRTSTYWLTRIQSFLYCNGNLGSFS	TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL	420	
31	133	3.3	1004	2	Q7Q4Q2		Q7Q4Q2 anopholes g						

RESULT 1
Q76B58 PRELIMINARY; PRT; 766 AA.
ID Q76B58; AC; DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DBCR1-1 like
GN Name=DBCRCRL;
Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Imoto I., Inzawa J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB11893; BAD04066.1; -
DR InterPro; IPR001862; MAC_PFF; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
DR SEQUENCE 766 AA; 8844 MW; D325EB7EF416FB3 CRC64;

Query Match 100.0%; Score 4081; DB 2; Length 766;
Best Local Similarity 100.0%; Pred. No. 2. 2e-285;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MINWRAGAEGLFSIMALNEWIAISLHCWLVAVAVSDOHA
1 MINWRAGAEGLFSIMALNEWIAISLHCWLVAVAVSDOHA
Db 1 MINWRAGAEGLFSIMALNEWIAISLHCWLVAVAVSDOHA
1 MINWRAGAEGLFSIMALNEWIAISLHCWLVAVAVSDOHA

61 TDFVDRSGESTRYKILPRAEFTPNIRLLGRPTL
61 TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL
61 TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL
61 TDVDRSGESTRYKILPRAEFTPNIRLLGRPTL

Qy	421	EETHSCTCPNDQVYCTAFLPCTVGDASACLTCAFDNRTRCGTNTGYMLSQGLICKPEVAE	480	DR SMART: SM00181; EGF: 1.
Db	421	EETHSCTCNDQVCTAFLPCTVGDASACLTCAFDNRTRCGTNTGYMLSQGLICKPEVAE	480	DR SMART: SM00457; MACPF: 1.
Qy	481	STDHYIGFSTDQDLEMKYLQLQKTDRLHEHALTFISNDMRLASWFDSWRKLMLTLKSN	540	DR SEQUENCE: 98.2%; Score: 4009; DB: 2;
Db	481	STDHYIGFSTDQDLEMKYLQLQKTDRLHEHALTFISNDMRLASWFDSWRKLMLTLKSN	540	DR Best Local Similarity: 97.8%; Pred. No.: 3.4e-280; Matches: 749; Conservative: 11; Mlematches: 6; Indels: 0; Gaps: 0;
Qy	541	KYSSLVLMILGSLQICLKNSKTLSTLEPVAVYNPFGSSHSESWMFVNENSSFPDWERTK	600	1 MIWRRAQAEFLSMLAWEWAISLHCWLAVAAVSQDAHATSPFDNLSDLKGDPFHRSQEY 60
Db	541	KYSSLVLMILGSLQICLKNSKTLSTLEPVAVYNPFGSSHSESWMFVNENSSFPDWERTK	600	1 MIWRRAQAEFLSMLAWEWAISLHCWLAVAAVSQDAHATSPFDNLSDLKGDPFHRSQEY 60
Qy	601	LDLPLQCYNWTLTGKWKTFETVTHYLRSRKSNGNGNESIYYPEPLEFDPSRNLY	660	61 TDFVDRSRQGSTRTCKYREFGRWKYNLNAYERNFLGSPLPLAPEFRTRLLGRPTL 120
Db	601	LDLPLQCYNWTLTGKWKTFETVTHYLRSRKSNGNGNESIYYPEPLEFDPSRNLY	660	61 TDFVDRSRQGSTRTCKYREFGRWKYNLNAYERNFLGSPLPLAPEFRTRLLGRPTL 120
Qy	661	MKINNIQVFGSMHFDPEAIRDLLQDLYPTQGSDSALQLEIRDRVNLSPQCQR	720	QY 121 QQTENLKKYGTFLSATLGGEESTLTVFKRKLSKRAGGSDSTNSSSVTLETLHQ 180
Db	661	MKINNIQVFGSMHFDPEAIRDLLQDLYPTQGSDSALQLEIRDRVNLSPQCQR	720	DB 121 QQTENLKKYGTFLSATLGGEESTLTVFKRKLSKRSESETNSSSVTLETLHQ 180
Qy	721	LDFSCLRHLKLSTSEVRIOQALQFNAKLPNTMDYDTTKLCS	766	QY 181 AASYFIRDSTLRRLLHHIQLASTAICLTETRTGPILOGSNYDNLDSSVVLQOSPENIQ 240
Db	721	LDFSCLRHLKLSTSEVRIOQALQFNAKLPNTMDYDTTKLCS	766	DB 181 AASYFIRDSTLRRLLHHIQLASTAICLTETRTGPILOGSNYDNLDSSVVLQOSPENIQ 240
RESULT 2				
QBKR9		PRELIMINARY;	PRT;	766 AA.
ID	QBKR9			
AC	QBKR9,			
DT	01-OCT-2002	(TREMBLe).	22,	Created)
DT	01-OCT-2002	(TREMBLe).	22,	Last sequence update)
DT	01-MAR-2004	(TREMBLe).	26,	Last annotation update)
DE	RIKEN cDNA B830045N13.			
GN	Name=B830045N13Rik;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10990;			
RN	[1]	SEQUENCE FROM N.A.		
RP	RC TISSUE-EYE;			
RC	MEDLINE=22308257;	PubMed=12477932;	DOI=10.1073/pnas.242603899;	
RA	Klauser R.D., Feinold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Strasberg R.L., Collins F.S., Wagner L., Shenm C.M., Schaefer C.F., Bhat N.K.,			
RA	Altschul S.F., Zeeberg B.R., Buetow K.H., Wang M., Saito S.I., Rubin G.M., Hong L.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Stapleton M., Soares M.B., Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,			
RA	Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,			
RA	Blakesley R.W., Logueillo N.A., Peters G.J., Abramson R.D., Mullahay S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettenman M., Medan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shvechko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]	SEQUENCE FROM N.A.		
RC	RC TISSUE-EYE;			
RA	Strasberg R.; Submitted (May-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC030498; AAH30498.1; -;			
DR	MGI: MGI:2443035; BB3045N13Rik.			
DR	InterPro: IPR00610; IEGF.			
DR	InterPro: IPR001862; MAC_perforin.			
DR	Pfam: PF01823; MACPF: 1.			
RESULT 3				
ID	Q8K1M7	PRELIMINARY;	PRT;	766 AA.
AC	Q8K1M7;			
DT	01-OCT-2002	(TREMBLe).	22,	Created)
DT	01-OCT-2002	(TREMBLe).	22,	Last sequence update)
DT	01-MAR-2004	(TREMBLe).	26,	Last annotation update)
DB	BMP_Retinoic acid-inducible neural-specific protein-3. Name=BRINP3;			
GN	Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OS				
OC				
OC				

Query Match									
Best Local Similarity		Score		DB 2:		Length		;	
Matches		748;		Pred. No.		2.1e-279;		Indels .	
P	A	SEQUENCE FROM N.A.							
A	A	Matsuoka I., Toda F., Nakatani T., Mori T., Ueno S., Kawano H.,							
A	A	Kobayashi M.,							
A	A	Submitted (JIN-2002) to the EMBL/GenBank/DBJ databases.							
R	R	EMBL; AB077854; BAC03100.1; - .							
R	R	InterPro; IPR006210; IECF.							
R	R	InterPro; IPR001862; MAC_perforin.							
R	R	PFam; PF0123; MACPF_1.							
R	R	SMART; SM00184; EGFP_1.							
R	R	SMART; SM00457; MACPF_1.							
Q	Q	SEQUENCE 766 AA; 88496 MW; 0D21705602E1EE5D CRC64;							
Query Match									
Best Local Similarity		98.0%		Score 3998;		DB 2:		Length 766;	
Matches		97.7%		Pred. No. 2.1e-279;		Indels .		Gaps 0;	
Conservative		10;		Mismatches 8;		;			
Matches 748;									
Y	Y	1 MIWRRAGELFSLMMALNEWMAISLHCWNLAVAVSDQHATSPFDWLISDKGPFFHSRQEY 60							
O	O	1 MIWRRAGELFSLMMALNEWMAISLHCWNLAVAVSDQHATSPFDWLISDKGPFFHSRQEY 60							
O	O	61 TDFVDRSROGSTRYKTRFGRMVKUNNLAVERRNFLGSPLAPEGFFRNLGRPRTL 120							
O	O	61 TDFVDRSROGSTRYKTRFGRMVKUNNLAVERRNFLGSPLAPEGFFRNLGRPRTL 120							
Y	Y	121 QQTENLTKYGHTFLLSATLGGEESLTIVFDKRKLSSRAEGSDSTTNNSSSYTLETHQL 180							
O	O	121 QQTENLTKYGHTFLLSATLGGEESLTIVFDKRKLSSRAEGSDSTTNNSSSYTLETHQL 180							
Y	Y	181 AASFYIDRDSTLRLHHQIASPAIKYVETRTOPLGCCNYNDLSVSVSLVQSPEPKIQL 240							
O	O	181 AASFYIDRDSTLRLHHQIASPAIKYVETRTOPLGCCNYNDLSVSVSLVQSPEPKIQL 240							
O	O	241 OGLOVLLPYLQERFVQALSYIACNSGEFICKENDWCHCSCPKEPCNCPSMDIQAME 300							
O	O	241 OGLOVLLPYLQERFVQALSYIACNSGEFICKENDWCHCSCPKEPCNCPSMDIQAME 300							
O	O	301 ENLRITETWKAYNSDFBESDEFPLFMRKLPFMMYFLNTSTIMHLWMDNSFORRYEOLN 360							
O	O	301 ENLRITETWKAYNSDFBESDEFPLFMRKLPFMMYFLNTSTIMHLWMDNSFORRYEOLN 360							
V	V	361 SMKOLFLRAQKIVTHKLFSISKRCHKQPLISLPRQRTSYWLTROISFLYCNENGJLGSFS 420							
O	O	361 SMKOLFLRAQKIVTHKLFSISKRCHKQPLISLPRQRTSYWLTROISFLYCNENGJLGSFS 420							
V	V	421 EETHSCTCPNDQVCTAPLPCVTDGASCLTCAPDNTRCGTCTGTGMLSQLCKPBEVAE 480							
O	O	421 EETHSCTCPNDQVCTAPLPCVTDGASCLTCAPDNTRCGTCTGTGMLSQLCKPBEVAE 480							
V	V	481 STDHYIGFTEDLDLEMYYLQKTDRLRREHALIFISNDMRNLSWDFSWRKMLLTLSN 540							
O	O	481 STDHYIGFTEDLDLEMYYLQKTDRLRREHALIFISNDMRNLSWDFSWRKMLLTLSN 540							
V	V	541 KYKSSLVNMILGSLQCLTKNSTLPLEVYVNPFCGSHSSWMEVNEUSFPDWERTK 600							
O	O	541 KYKSSLVNMILGSLQCLTKNSTLPLEVYVNPFCGSHSSWMEVNEUSFPDWERTK 600							
O	O	601 LDEPLQCTNWLTLGNIKKTFFSTVHYLRSRIKSNGNGNESIYYPELEFDPSNLGY 660							
O	O	601 LDEPLQCTNWLTLGNIKKTFFSTVHYLRSRIKSNGNGNESIYYPELEFDPSNLGY 660							
O	O	661 MKINNIIQFGYSFHDPFAIRDILQDQDYLQDQDYLQDQDYLQDQDYLQDQDYLQDQ 720							
O	O	661 MKINNIIQFGYSFHDPFAIRDILQDQDYLQDQDYLQDQDYLQDQDYLQDQDYLQDQ 720							
V	V	721 LDIFSCURHRHLKLSTSVRVLQSALOFNAKLPTNTMDYDTTRKLCS 766							
O	O	721 LDIFSCURHRHLKLSTSVRVLQSALOFNAKLPTNTMDYDTTRKLCS 766							

SQ	SEQUENCE	781 AA;	882145 MW;	DFF3EB83A088B599 CRC64;	[1]
	Query Match	72.6% Score: 2962; DB 2; Length: 781;			
	Best Local Similarity	70.6% Fred. No. 1.1e-204;			
	Matches	543; Mismatches 99; Conservatve 99;			
Qy	16 ALIWEW-IAISLHCMVLAIA-----VSQDHAT---SPFDWLISDKGPFRSQEYTD 63	4;			
Db	13 AVAPFTALLAQLPGRVLAISATAAVVPEQHSAYAGQHLDWLTDRGFHRQAQBYAF 72				
Qy	64 VDRSKQFSTRYKTYREFGRMVNAIAVERNFGLSPPLAYPEPFNRIRLGRERPLQQI 123				
Db	73 MERYQGFITRYRITREFAWKVNLAERKDFFSLPLPAPEFIRNIRLGRPNLQQV 132				
Qy	124 TENLIKKYGTHFLISATLGGESESLTIFVDKRLSKRAEGSDSTT-----NSSSVTLET 177				
Db	133 TENLIKKYGTHFLISATLGGESESLTIFVDKQLGRKTETGGASLTIGGSNSNTAVSLET 192				
Qy	178 HOLASYFTIRDSTLRLHQIASTAIKUTETRGPIGCSNYDNLDSVSSVLYQSPEK 237				
Db	193 HOLASYFTIRESTRLRLHQIASTAIKUTETRGPIGCSNYDNLDSVSSVLYQSPEK 252				
Qy	238 IQLQGIVLPLDYLDRFVQALSYTAACNSEGEFLICKENDCWCHCGPKFPECNCPMSDIO 297				
Db	253 VQLLGIVLVLPEYLRLRFVAAALSYTCSSEGELVKENDCWCKCSPTPCECNCPDADIQ 312				
Qy	298 AMEENILRLRTETWKAYSDEESEDEFKLMKRLPMNMFYLTNSTIMHLNTMDNSNQRRYEQ 357				
Db	313 AMEDSLLQIQDPSWATHNRPBESEFEQALIKRLPDRFINSTAISQFWMDTSQHRYQQ 372				
Qy	358 LENSKQQLFLKAQKIVHKLFSKRCHKQPLISLPRQTSTYLTROSFLYCNENGLL 417				
Db	373 LGAGHVYKVLPKTRTHLRLFLCVRCHRQFLPKERSUYYNNRQIQLYCGESTTFPG 432				
Qy	418 SFSEBTHSCTCPNDOVVCTAFLPCTVGASACLTCAPIRDNRCTCNTQYMLSGLCKPE 477				
Db	433 TELOSHSTSCTCPYDOSSCQGPICPALEGPACAHCAPDNSTRCSNCNPQVYLAQGLCRF 492				
Qy	478 VAESTDHYIGFETDLDLEMKYLQKTLKNTSLPVALVYNNPRPGGSHSESWMVPVNNSFPDME 537				
Db	493 VAESTLENFLGLETDLQDLELKYLQKDSRIEVHSIIFSNDRMIGSWFDPSWKRMLLT 552				
Qy	538 KSNKYKSSLVHMLGSLQCLTKNTSLPVALVYNNPRPGGSHSESWMVPVNNSFPDME 597				
Db	553 KSNKYKSSLVHMLGSLQCLTKNTSLPVALVYNNPRPGGSHSESWMVPVNNSFPDME 612				
Qy	598 RTKEDLPLOCYNTWLTLGKWKWTFFETHYLRLSRKIKNGPNNGNESIYEPLEPIDPSRN 657				
Db	613 RTNYDAAAQCQNWTITLGNRWKTFETVHVLRLRIKSLSDDSSNETIYEPLEMIDPSKN 672				
Qy	658 LGYMKINNIQFGSMHFDEAIRDLLQDLYDPTYQGSDSALLQLEIRDRYNKLSPPG 717				
Db	673 LGYMKINTIQLFGYSLPFDDEAIRDLLQDLYDPTYQGSDSALLQLEIRDRVNQLSPG 732				
Qy	718 QRRDLDFSLCILRHRLKLSTSEVYRQSLQAFANAKLPLNTMDYDTTKLCS 766				
Db	733 KVRDLDFSLCILRHRLKLANNEVGTQSSRFAFNKLPLPVVEYTGKLCs 781				
RESULT 7					
QBN360	PRELIMINARY;	PRT;	783 AA.		
AC	QBN360;				
DB	01-OCT-2002 (TREMBLre1_22, Created)				
DB	01-OCT-2002 (TREMBLre1_22, Last sequence update)				
DB	25-OCT-2004 (TREMBLre1_28, Last annotation update)				
DE	BMP/retninoic acid-inducible neural-specific protein 2 (DBCCR1-DE like2).				
GN	Name=KIAA1741; Synonyms=DBCCR1L2;				
OS	Homo sapiens (Human); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	Liensmkolflkaqkivhklfslskrchkqplislprrtstwtriosflycnenglg				
NCBI_TaxID	=3606;				

Db	375	LGAGLKVDFKTHRILRLFLNLCRKHRQPRFLPKERSLSYWNRNRIQSLLLYGEESTFPG	434	Qy	235	ENKIQIQLGQVLLPDMIQLERIVQAALSYIACNSEGFIICKENDCWCICHGPKFPECNCPSM	294
Qy	418	SFGSETHSCTCPNDQVCTAFLPCTVGRASACTCAPDNTRGCTCNCGMISQGLCKPE	477	Db	252	ENKVQLLGLQVLPENLRRERVAATIYTTSSEGVRENDCWCKCSPPPPECNPDA	311
Db	435	TPEQSHSCTCPYDQSSCGPITCALGERGPRCAHCAPDNSTRGCSNPGYTAQGLCRPE	494	Qy	295	DIQAMERNLIRITETWAKNSDFEESEDEFKLFMKRLPMLNYFLNTSTIMHLWTMDSNFORR	354
Qy	478	VAASSTDHYIGFTEDLQDLEMKLLQKDERRIEWAIFTSNDNRLNSWFDPSYRKRMLLT	537	Db	312	DIQAMERSLLQDQSVAATHANQEESEEFQTLKRSRDRFLNSTAQYWWMDANQHQR	371
Db	495	VASSELENPLUGLEDTDLQDLEKYLQKQDSRTEVHSATISITSNNMBLGSDPSYRKRMLLT	554	Qy	355	YEQLENMKQULFKAQKIVHKLFSLSKRCHQKPLSLPROQTSTYNTBIOSEFLYCHENG	414
Qy	538	KSNKVKSSLVHMMLGSLQICLTKTNSTLEPVLAIVYNNPFGGSHSESNFMPYNENSFDWE	597	Db	372	YCOLGLASLKVLLKQHRIIVRFLNLCKRCHQPRFRPKERSLSFWNRIQSLLYCBST	431
Db	555	KSNKVKKGPLVHVNLALSIQCLTKTNSTLEPVNAIVYNNPFGGSHSESNFMPYNEGSFWDWE	614	Qy	415	LIGSFSEBETHSCTCPNDQVCTAFLPCTVGDASACLTACPDNRTRCTCNCGMLSGLC	474
Qy	598	RTKLDLPLQCYNTWLTLCNGWKTFEFFTWHYLRSRKSNGNESTYYPLEFLIDPSRN	657	Db	432	FPGTEFLQSHSCTCPYDQSSQQGP1PCA1G3GPACAHASCUDNTTGSNCNPSYVLAGQLC	491
Db	615	RTNVDAAACQWNMTITLGNRWTFFETVHVVYURSRKSLSDDSNETTYYPELMDESKN	674	Qy	475	KPEVASTDHYTGFETDQLDMEKYLQKTDRIEYHAIFIISNDMFLNSWFDPSWKRML	534
Qy	658	IGYMKINNIQVFGYSMEHDPEAIRDLLQDQDYPTQTSQSDSALLQLETRDVKNLSSPG	717	Db	492	RPEVAASLENFLGLETDLQDLEKYLQKRSRHSIEHSIFISNDMFLGSWFDPSWKRML	551
Db	675	IGYMKINNLQVFXSLARDLQDQDYPTQTSQSDSALLQLETRDVKNLSSPG	734	Qy	535	LTLKSNKVKSSLVHMMLGSLQICLTKTNSTLEPVLAIVYNNPFGGSHSESNFMPVNENSF	594
Qy	718	QRIDLFLFCLLRHRLKUSTSEVRIOQSAQAFNKLPTMDYDTTKLCS	766	Db	552	LTLKSNKVKSSLVHMMLGSLQICLTKTNSTLEPVMAIVYNNPFGGSHSESNFMPVNENSF	611
Db	735	KYRDLFLSCLLRHRLKLANNEVGIQSSLRAFNSKLPNPVEYETGKLCS	783	Qy	595	DWERTKLDPQCYNTWLTLCNGWKTFEFFTWHYLRSRKSNGNESTYYPLEFLIDP	654
Db	78	RESULT	9	Db	612	DWERTNDAAAQCONWTITLGNRWTFFETVHVVYURSRKSDDSENNTTYEPLNTDTP	671
Q8K1M8	PRELIMINARY;	PRT;	783 AA.	Qy	655	SRNLGYMKINNIQVFGYSMEHDPEAIRDLLQDQDYPTQTSQSDSALLQLETRDVKNLCS	714
ID	Q8K1M8,	PRELIMINARY;	PRT;	Db	672	SKNLGYMKINNLQVFGYSLPDPDPAIRDLLQDQDYPTQTSQSDSALLQLETRDVKNLCS	731
AC	Q8K1M8,	PRELIMINARY;	PRT;	Qy	715	PGORRDLFLSCLLRHRLKUSTSEVRIOQSAQAFNKLPTMDYDTTKLCS	766
DT	01-OCT-2002	(TREMBLrel.	22; Created)	Db	732	PGKVRDLDLFLSCLLRHRLKLANNEVGIQSSLRAFNSKLPNPVEYETGKLCS	783
DT	01-OCT-2002	(TREMBLrel.	22; Last sequence update)	Qy	783 AA;	SEQUENCE FROM N.A.	
DE	01-MAR-2004	(TREMBLrel.	26; Last annotation update)	Qy	99	SEQUENCE FROM N.A.	
GN	Name=RINP2;			Qy	99	SEQUENCE FROM N.A.	
OS	Rattus norvegicus (Rat)			Qy	99	SEQUENCE FROM N.A.	
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;			Qy	99	SEQUENCE FROM N.A.	
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Murinae; Rattus.			Qy	99	SEQUENCE FROM N.A.	
OX	NCBI_TAXID=10116;			Qy	99	SEQUENCE FROM N.A.	
RN	[1]			Qy	99	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.			Qy	99	SEQUENCE FROM N.A.	
RA	Matsuoka I., Ueno S., Nakatani T., Toda F., Mori T., Kawano H.,			Qy	99	SEQUENCE FROM N.A.	
RA	Kobayashi M.;			Qy	99	SEQUENCE FROM N.A.	
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			Qy	99	SEQUENCE FROM N.A.	
DR	EMBL; AB077853; BAC03099.1;			Qy	99	SEQUENCE FROM N.A.	
DR	IPRO006210; IPRO006212; IEGF.			Qy	99	SEQUENCE FROM N.A.	
DR	InterPro; IPRO01862; MAC_Perforin.			Qy	99	SEQUENCE FROM N.A.	
DR	Pfam; PF01823; MACPF; 1.			Qy	99	SEQUENCE FROM N.A.	
DR	SMART; SMART00481; EGF; 1.			Qy	99	SEQUENCE FROM N.A.	
DR	SMART; SMART00457; MACPF; 1.			Qy	99	SEQUENCE FROM N.A.	
SQ	SEQUENCE	783 AA;	89138 MW;	Qy	99	SEQUENCE FROM N.A.	
		2FF29532F62975D CRC64;		Qy	99	SEQUENCE FROM N.A.	
Query Match	72.6%	Score 2962;	DB 2;	Qy	99	SEQUENCE FROM N.A.	
Best Local Similarity	70.7%	Pred. No. 1..1e-204;		Qy	99	SEQUENCE FROM N.A.	
Matches	546;	Conservative 97;	Mismatches 107;	Qy	99	SEQUENCE FROM N.A.	
		Indels 22;	Gaps 5;	Qy	99	SEQUENCE FROM N.A.	
Qy	17	LN---EW---TALSIIQHVLAVA---	-VSDQHATS---	Qy	60	TDIVDRSRQGFSTRYKTYREFGRWKVNLLAVERRNFLGSSPLLAPEPFRNTRLLGRPRL	120
Db	12	LWPEAAPAVVLLGVPGWVLAWSATVAAVPEQHVSSAGQAPLDWLITDGPFHRAQEY	71	Db	72	ADEFMRQGFTTRYKTYREFARWKVNLLAERKDFPSLPLAPEPFRNTRLLGRPRL	131
Qy	61	TDVDRSRQGFSTRYKTYREFGRWKVNLLAVERRNFLGSSPLLAPEPFRNTRLLGRPRL	120	Qy	121	QQTENLIKKYGHFLLSATLGGEESTTIVFDKRLSKRAEG----SDSTNNSSVTL	174
Db	72	ADEFMRQGFTTRYKTYREFARWKVNLLAERKDFPSLPLAPEPFRNTRLLGRPRL	131	Db	132	QQTENLIKKYGHFLLSATLGGEESTTIVFDKRLSKSETLGGYPVVGTTGNSSAVL	191
Qy	175	ETLHOLASASYIDRDSTLRRHIIQIASTAKVTEETGPIGCSNYDNLDYSSVLYQSP	234	Qy	121	ETLHOLASASYIDRDSTLRRHIIQIASTAKVTEETGPIGCSNYDNLDSSVSVLQSP	251
Db	192	ETLHOLASASYIDRDSTLRRHIIQIATGAIKVTETGPIGCSNYDNLDSSVSVLQSP	251	Db	16	ALWEW--IAISLHCVLVAYA-----VSDDHAT---SPWDWLISDKGPFRHSQBYTDF	63

RESULT 11					
	Q72ZR3	PRELIMINARY;	PRT;	761 AA.	
RA	Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases				
DR	AK123336; BAC855533.1; -				
DR	Inter-Pro: IPR011823; MAC_perforin.				
PFam	PF01823 / MACPF_1.				
DR	SMART: SR00457 / MACPF_1.				
DR	SEQUENCE: 678 AA; 76520 MW; F34E4C754AC2612C CRC64;				
Qy	133 THFLSATLGGEESLTIVDVKRKLSKAEGSDSTT-----NSSSVY				
Best Local Similarity 60.6%; Score 2474.5; DB 2; Length 70.5%; Prod. No. 1..3e-19; Mismatches 86; Indels 451; Conservative 86; Mismatches 96; InDel 1.					
Db	40 INTLVFTI-GEEBLTIVDKQLGRKTTETGGASIIGGSNSTAVS				
Qy	187 DRDSTLRLLHIIQIASTAIKVTETRTCPLGCSNYDNIDSVSSVLYQS				
Db	99 DREBTLRLLHIIQIASTAIKVTETRTCPLGCSNYDNIDSVSSVLYQS				
Qy	247 LPDYQERTVQALLSYIACNSCEFIGENDWCHCCPKPBCNCPS				
Db	159 LPEYLRLRERVAALSYITCSCSEBLVCKENDCWCKCSPTPECNCPD				
Qy	307 TETWKAYNDSFEESDEFKLFMGRMLPNHYFLNTSTIMLWTMDNSFOR				
Db	219 QDSWATHANRQFEESEEFOALLKRLPDRFLSTAISCFWAMTSLOH				
Qy	367 LKAQKIVHKLFSLSKRCHKQPLJSLPQRTSTYWLJPIOSFLCYNEN				
Db	279 KCTHRILRLFLNICKRHRQPRFRPLVERSLYYWRNRIQSLIYCGES				
Qy	427 TCNDQVQVTAFLPCTYGDASACLTCAPDNRTRCGTGTGNYLSQLG				
Db	339 TCPYDQSSCOQGPICPALEGPAHCPDNSTRCGSNPGVYLAQGL				
Qy	487 GFETDLDQLEMKYLQLQCDTRREVHAIFISNDMRNLNSWFDSWRKRM				
Db	399 GLETDLQLEMKYLQLQCDSRREVHSFISNDMRNLSSWFDSWRKRM				
Qy	547 VHMILGLSLQCICTKNTSTLEPLVAYVNPFGGSHSESWMPVNENSP				
Db	459 VHMILGLSLQCICTKNTSTLEPLVAYVNPFGGSHSESWMPVNENSP				
Qy	607 CYAWTLTGKWKTPPTVHYLRSRKSGPNGNESIYXPLEFID				
Db	519 CQWTITIGRNKTKTFVTWYHLRSRKSLDDSSNETIYXPLEMTD				
Qy	667 QVEGYSHEFDPEAIRDILQLDQPTYQGSDSALLQLEIRDVNL				
Db	579 QVEGYSPEFDPEAIRDILQLDQPTYQGSDSALLQLEIRDVNL				
Qy	727 LLRHLKLSTSEVRYICOSALQAFNAKLPNTMDYDTTKLCS 766				
Db	639 LLRHLKLANNEVGRQSSURAFNSKLPNPVBYETGKLC 678				

RC	TISSUE=Brain;	DT	01-AUG-1998 (TREMBurel. 07, Created)
RA	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.	DT	01-AUG-1998 (TREMBurel. 07, Last sequence update)
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.	DE	01-MAR-2004 (TREMBurel. 26, Last annotation update)
DR	EMBL; AJ551161; CAD90040.1; -	RA	IB3089A.
DR	GO: GO:0005515; F:protein binding; ISS.	GN	Name=IB3089A;
DR	GO; GO:00019; P:cell cycle; ISS.	OS	Homosapiens (Human)
DR	GO; GO:000219; P:cell death; ISS.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	InterPro: IPR001862; MAC_perforin.	M	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
DR	SMART; SMD0457; MACPF; 1.	CX	NCBI_TaxID=9606;
DR	Pfam; PF01823; MACPF; 1.	RN	[1]_TaxID=9606;
DR	SEQUENCE 761 AA; 88792 MW; 8D0B03F5910D1473 CRC64;	RP	SEQUENCE FROM N.A.
Query Match	53.5%; Score 2184; DB 2; Length 761;	RC	SEQUENCE=Brain;
Best Local Similarity	52.8%; Pred. No. 1.3e-148;	RX	MEDLINE=98207242; PubMed=9545632; DOI=10.1006/geno.1997.5165;
Matches 410; Conservative 134; Mismatches 205; Indels 28; Gaps 10;		RA	Habuchi T., Luscombe M. Elder P.A.; Knowles M.A.; "Structure and methylation-based silencing of a gene (DBCCP1) within a candidate bladder cancer tumor suppressor region at 9q32-q33.";
Qy	1 MIWRSRAGAEFLSMALWENIALS-LHCWVLAVAAYSDOHTSPFDWLSSDKGPFRHSQE 59	RT	Genomics 48:277-288 (1998).
Db	1 MNWRL---VFLYLLFIWHDHLLVQPSH---QDPAATNQHISKEFWLISRGPFHHSRS 53	DR	EMBL; AF027734; AAC39691.1; -.
Qy	60 YTDDEVDSRQSFSTRYKLYREFCPRWIKNNTLAVERRNFLGSSPLAPBEFFNRIRLGRPT 119	PIR	PIR; T09052; T09052.
Db	54 YLSFVERHRQGFTTRYKLYREFARWKVNTTTERDNLHNLPLMPEFOSIRIILGRPT 113	DR	GO; GO:0005515; P:protein binding; IPI.
Qy	120 IQQITENLIKIGTHFLSATLGESLTLIVDVKRLSLKRAEGSDSTTNSSVTLETLHQ 179	DR	GO; GO:0007049; P:cell cycle; NAS.
Db	114 TQQFIDTTIKYKGTLLSATLGGEAIIQDPSKQATOSBALHQ 166	DR	GO; GO:0008219; P:cell death; NAS.
Qy	180 LAASYFIDRDSLTRLHLHQIASTAIKVTETRGPGLCSNYDNLDSSVSYLVQSPENKIQ 239	DR	InterPro: IPR001862; MAC_perforin.
Db	167 LASSYFYDRTGMTRHLHQIASTGAKVTETRGPGLCSNDLNLDSSVSYLVQSTESKLH 226	PFam	PF01823; MACPF; 1.
Qy	240 LOGQLVLPDYLQERFYQAAALSYIACNSEGFEICKENDCNGCHGPKPEPECNCPMSDIQAM 299	DR	SMART; SN00457; MACPF; 1.
Db	227 LGQLQIIFPQLQEKVQSAISYIMCNGEGYICRNSQCGQCAEFPPCNCIPTDIQIM 286	DR	SEQUENCE 761 AA; 88790 MW; 59E1B2B31353E5 CRC64;
Qy	300 EENLRLRITETKAYNSDFEESDEPKLEMKRPLMYFLNTSTIMHLWTMDSNFORRYEQLE 359	Qy	1 MIWRSRAGAEFLSMALWENIALS-LHCWVLAVAAYSDOHTSPFDWLSSDKGPFRHSQE 59
Db	287 EYTLANMAKTVTEAYKDLENSEFESFMKRPSPNHLTLIASIHQWGNDDQMLQRYKLQ 346	Db	1 MNWRL---VFLYLLFIWHDHLLVQPSH---QDPAATNQHISKEFWLISRGPFHHSRS 53
Qy	360 NEMKQFLKAOKVXVHLFLSSLRKCHKPLISIIPROSFTWLTRIOSFLYCNENGILGSF 419	Qy	60 YTDDEVDSRQSFSTRYKLYREFCPRWIKNNTLAVERRNFLGSSPLAPBEFFNRIRLGRPT 119
Db	347 SSLEAQQRQKIRTARKULFGSVCYCRNPNHQPRETTIQMUTRIOSLILYCNENGFWGTF 406	Db	114 TQFIDTTIKYKGTLLSATLGGEAIIQDPSKQATOSBALHQ 166
Qy	420 SEETHSCTCPNDQVYCTAELPCVGDASACLTCAPDNRTRGTCNTGYMLSGQICKPEVA 479	Qy	180 LAASYFIDRDSLTRLHLHQIASTAIKVTETRGPGLCSNYDNLDSSVSYLVQSPENKIQ 239
Db	407 IESQRSCVCHGTSCLCORPIIIGNNSCAMCSLANSISLGSCNRGYKLYRGRCBEPQNV 466	Db	120 LQQTENLIKYKGTLLSATLGGEESLTIFVDRKRLSKRAEGSDSTTNSSVTLETLHQ 179
Qy	480 ES-TDHYIGETDL-QDLEMKYLQKTDRLRVEHAIFISNDMLNWSDPSWKRMLL 535	Qy	121 MNWRL---VFLYLLFIWHDHLLVQPSH---QDPAATNQHISKEFWLISRGPFHHSRS 53
Db	467 DSERSEQFISPTDQDQDLEKLYQKMDRLYVHTTSENEIRDTFFFPRWKRMSL 526	Db	114 TQFIDTTIKYKGTLLSATLGGEAIIQDPSKQATOSBALHQ 166
Qy	536 TLKSNKYKSSVHMLGSLQICLTKNSTLBEVLAVYVNPFGSHSESWMPVNENSFPD 595	Qy	300 BENLRITETKAYNSDFEESDEPKLEMKRPLMYFLNTSTIMHLWTMDSNFORRYEQLE 359
Db	587 WEKIRLQ-NSCYNWNLLGRWKTETVYLRSRTRLLNET-GGPVDSLSDPS 644	Db	347 SATEQRQKORTARKLFGLSVRCHNPNHOLPQERTIQMLARYVNLQYNGFWGTF 406
Qy	656 RNLYGMKINNQVEGYSMHFPDRAIRDLLQDLYPTIQGQ --- DSALLCOLLEIRDRVN 711	Qy	287 EYTLANMAKTVTEAYKDLENSEFESFMKRPSPNHLTLIASIHQWGNDDQMLQRYKLQ 346
Db	527 TLKSNKRNMDPHMVIGISMRCOMRNSSLPMFFVYVNPFGSHSESEGNNMPFGEXYPR 586	Db	407 LESQSRPFLPPQYKPLQKPLISLPRORTSTYWLTRQSFLYCNENGILGSF 419
Qy	596 WERTKUDLPQOCYNNWLTGKMKWTETVYLRSRIKSNGPQNGNESTYYPELEPFDPS 655	Qy	360 NSMKOLFQAKVHLFLSSLRKCHKPLISIIPROSFTWLTRIOSFLYCNENGILGSF 419
Db	587 WEKIRLQ-NSCYNWNLLGRWKTETVYLRSRTRLLNET-GGPVDSLSDPS 644	Db	227 LQGLQVLPDYLQERFYQAAALSYIACNSEGFEICKENDCNGCHGPKPEPECNCPMSDIQAM 299
Qy	645 ERQFYKISDQYGVGSLRFRADLURSAQDVYNOSTGGDFYSSVMMULLDRDRN 704	Qy	300 BENLRITETKAYNSDFEESDEPKLEMKRPLMYFLNTSTIMHLWTMDSNFORRYEQLE 359
Db	712 FLSP---PGQRDLESCLLRLRKLUSTEVNRQISALQAFNAKLPNTMDTTKLC 765	Db	347 SATEQRQKORTARKLFGLSVRCHNPNHOLPQERTIQMLARYVNLQYNGFWGTF 406
Qy	712 FLSP---PGQRDLESCLLRLRKLUSTEVNRQISALQAFNAKLPNTMDTTKLC 765	Qy	420 SEETHSCTCPNDQVYCTAELPCVGDASACLTCAPDNRTRGTCNTGYMLSGQICKPEVA 479
Db	705 FLAPPVAPGKPOLDLFSCLMLKHLRKLUTNSELIRVNHADLYNTEILKQSDOMTAKLC 761	Db	467 DSERSEQFISPTDQDQDLEKLYQKMDRLYVHTTSENEIRDTFFFPRWKRMSL 526
RESULT 12	PRELIMINARY;	Qy	536 TLKSNKYKSSVHMLGSLQICLTKNSTLBEVLAVYVNPFGSHSESEGNNMPFGEXYPR 586
ID 060477	PRELIMINARY;	Db	527 TLKSNKRNMDPHMVIGISMRCOMRNSSLPMFFVYVNPFGSHSESEGNNMPFGEXYPR 586
AC Q60477;	AA.	Qy	596 WERTKUDLPQOCYNNWLTGKMKWTETVYLRSRIKSNGPQNGNESTYYPELEPFDPS 655

Db	587	WEKIRLQ-NSQCTNWTLGLNRWKTFFPTVHRYLRSRTRLPTLRLNET-GQGPVDSLSDPES	644		Db	114	TQQFIDTTIKKYGTHLLISATLGGEALTYMDKSRLL-----DRKSGNATQSVERLHQ	166
Qy	656	RNLGYMKINNIQVGYSMHFDPEAIRLILQLDQYPTQGSQ---DSALLOLLEIRDVN	711	Qy	180	LAASYFTIDSTLRLRHIOJASTAIKVTETRGPICCSNYDNLDSSVSVLYQSPENPKIQ	239	
Db	645	KRQGYTQDLSQVFGYSLRNFADLRLSAVQVNQSTGGQFYSSSSVVMILLDIRDRIN	704	Db	167	LASSYFVDRTDCTMRLHEIQIISGIAKVTETRGPICNS-DNLDSVSVLQSTERKLH	226	
Qy	712	KUSP---PGQRRLDLFSCLLRLKUSTSEVRQSOAFLQAFNKLNTMDYTTLKC	765	Qy	240	LOGLOVLLPDYLQERFVQAALSYTACNSEEFIGKENDDCMGCHGPKPECNCPSPMDIQAM	299	
Db	705	RLAPPVAPGKPKQDLDLFSCLMLKHLKLTNSEITRVNHALDLNTEILKQSDOMTAKLC	761	Db	227	LGLOLQIFPQLQERFVQAALSYTACNSEEFIGKENDDCMGCHGPKPECNCPSPMDIQAM	286	
RESULT 13								
Q6P1AO	PRELIMINARY;	PRT;	761 AA.	Qy	300	BENLRITETWKAYNSDFEESDEFKLFLMRPLPMNYPFLNTSTIMHLWMTDSNFQRYYEQLE	359	
ID				Db	287	EYTLANMAKSWAAYKDLENSDEFKSFKLPLSNHFLTIGSIIOHNGNDWPLQNRXKLLQ	346	
AC	Q6P1AO;			Qy	360	NSMKOLFIAKQIVKLFSLSKRCKHQPLISLPRORTSTWLTRIQSFLYCNENGLLGSF	419	
DT	05-JUL-2004	(T-EMBL)rel.	27, Created)	Db	347	SATEAQRKQIORTARKLFGISVRCHNPQHPLPRTIQQMLARYQSLLYCNEGFWGT	406	
DT	05-JUL-2004	(T-EMBL)rel.	27, Last sequence update)	Qy	420	SEETHSCTCPNDNOVYCTAFLPCTVGDASAGLTCAPDNTRCGTCNTGMLTSQGLCKPEVA	479	
DE				Db	407	LESQSRSCVGHGSTLQCQPICVGNNNSAMCSLANSIUCGSCNKYKQYGRCEPQNV	466	
GN	Name=dBC1;			Qy	480	ES--TDHYIGFETDL-ODLEMKYLQLQTRRIEVHAIFISNDMRLNLSWEDPSWRKRM	535	
OS	Homo sapiens (Human);			Db	467	DSERSEQFISFETDLDPODILEKYLQKNDLSRVLVHTTFISNEIRLDTFFDPWRKRM	526	
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			Qy	536	TLKSNKRYKSSLVHMLGLSLQICLTKNSTEPVLAIVNYPFGGSHSESWMPVNENSFPD	595	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	527	TLKSNKNRMDFIHMVIGMSRICQMRNSLSDPMFVYVNPFGGSHSEGMMPFGEGYPR	586	
OX	NCBI_TaxID=9606;			Qy	596	WERTKLDPLOCNTWLTTLGKWKNTFFETPYHIYLRSRKSNGPNCGNESTYYPELEFDI	655	
RN	[1]			Db	587	WEKIRLQ-NSQCTNWTLGKWKTFETVHRYLRSRSLTPLRLNET-GQGPVDSLSDP	644	
RP	SEQUENCE FROM N.A.			RA	544	DIATCHENKO L., Marusina K., Farmer A.A., Grouse L.H., Dergue J.G.,		
RC	TISSUE=Brain;			RA	522	Strausberg R.L., Fengold E.A., Grouse L.H., Dergue J.G.,		
RX	MEDLINE#12477932; PubMed#124603899;			RA	503	Klausner R.D., Collin F.S., Wagner L., Schuler G.D.,		
RA	5-12			RA	484	Aitschul S.D., Zeeberg B., Buston R.K., Shearer C.M., Bhat N.K.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last sequence update)	RA	465	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	446	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	427	Stapleton M.B., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	408	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	389	Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahay S.J.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	370	Bobas S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	351	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	332	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Kettman M., Young A.C., Shevchenko Y., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	313	Jones S.J., Marra M.A., Smallius D.E., Schein J.E., Jones S.J., Marra M.A., Schein J.E.,		
RA	05-JUL-2004	(T-EMBL)rel.	27, Last annotation update)	RA	294	RT "Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences";			RA	275	RT "Generation and initial analysis of more than 15,000 full-length human		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			RA	256	RT "Generation and initial analysis of more than 15,000 full-length human		
RN	[2]			RA	237	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.			RA	218	RC TISSUE=Brain;		
RC	STRASBURG R.;			RA	200	RA STRASBURG R.; Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.		
RA	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			DR	181	DR EMBL: BC065196; AAB65196; -.		
DR	InterPro; IPR01862;			DR	162	DR Enriched library, clone: B20017A03 Product: deleted in bladder cancer		
DR	InterPro; IPR01862;			DR	143	chromosome region candidate 1 (human); full insert sequence (Deleted		
DR	SMART; SM00457; MACPF_1.			DR	124	DR Name=dBcr1; Cancer chromosome region candidate 1.		
DR	SMART; SM00457; MACPF_1.			DR	105	DR Name=dBcr1; Synonyms:BRINP; Mus musculus (Mouse).		
DR	SEQUENCE FROM N.A.			OC	86	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RT	Best Local Similarity 52.3%; Score 2161; DB 2; Length 761;			OC	85	OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus		
RT	Matches 406; Conservative 134; Mismatches 209; Indels 28; Gaps 10;			RN	84	RN SEQUENCE FROM N.A.		
Qy	1 MINIWSRAGAEFLSMALMEWIALS-LHCVLVALDAVSQDHATSPDWLISDKGPFRHRSQE			RC	83	RC TISSUE=Brain;		
Db	1 MNWRF--VLLYLFINGRISVQSPHS---QEPAGTDOHVSKEDFWLISDKGPFRHRS			RA	82	RA STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
Qy	60 YTDFVDRSRQGFSTRYKIYREFGRWVNLAVLAVERRNFLGSPPLAPEFEFRNLGRERP			RA	81	RA Ariga H., Arai N., Abe A.; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
Db	54 YLSVERHRHQFTRKYREFARWKVRNTAIEFRDLYRHPVPMPEFORSTRLGRERP			RJ	80	RJ SEQUENCE FROM N.A.		
Qy	120 LQQITENLIKKYGTHELLSATLGGEESLTIVFDKRLSKRAEGSDSTNNSSVTLHQ			RC	79	RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;		
Db	54 YLSVERHRHQFTRKYREFARWKVRNTAIEFRDLYRHPVPMPEFORSTRLGRERP			RA	78	RA RN 99219253; Published: 01-10-2001; DOI=10.1016/S0076-6879(99)03004-9;		
Qy	120 LQQITENLIKKYGTHELLSATLGGEESLTIVFDKRLSKRAEGSDSTNNSSVTLHQ			RA	77	RA Carninci P., Hayashiaki Y.; "High-efficiency full-length cDNA cloning.";		

- RL Meth. Enzymol. 303:19-44(1999).
 [3] RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RC MEDLINE=21085660; PubMed=11217831; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [4] RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RC MEDLINE=20493974; PubMed=1042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayashizaki Y.;
 RA Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5] RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RC MEDLINE=20530913; PubMed=1107681; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., NagaoKA S., Sasaki N., Carninci P.,
 RA Kondo H., Akiyama J., Niishi K., Kitaunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura M., Nishime T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Matsuura T., Tanaka T., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system 384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6] RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RC MEDLINE=12477932; PubMed=10.1073/pnas.242603899;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W.,
 RA Hayashiida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirczane T.,
 RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
 RA Katoch J., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazaki N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akaiwa S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashiizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 [7] RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RC MEDLINE=12477932; PubMed=10.1073/pnas.242603899;
 RA Strasberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loqueilano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,
 RA Villalba D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
- RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 Jones S.J., Marr A.M.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Brain;
 RC Director MGC Project;
 RA Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
 RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB00589; BAB37001..1..;
 DR EMBL; AK045420; BAB32355..1..;
 DR EMBL; BC079630; AAH79630..1..;
 DR MGD; MGI:1928478; Dbcrc1.
 GO; GO:0005615; C:extracellular space; TAS.
 GO; GO:0005515; F:protein binding; ISS.
 GO; GO:0007049; P:cell cycle; ISS.
 GO; GO:0008219; P:cell death; ISS.
 PFam; PF0183; MACPF..1..;
 SMART; SM00457; MACPF..1..;
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 DB 1 MNWRF--VEYLFLFWGRGISVQPS--RQBAGTDQHYSKFEFDWLISDGPFHHSRSY 54
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 DB 55 LSFVVERHRQGPSTRYKRYREFARVTRVNTAERDOLRVPHVPLMFBQRSPRTRLLGRPTT 114
 Qy 121 QQITENLKKYKGTHFLSATUGGEESLTIYDVKRLSKRAGSDSTTNSSSVTLETQLH 180
 DB 115 QQFIDTIIKKYKGTHFLSATLGGEBAALTMMDKSRL-----DRKSGNATOSVEALHOL 167
 Qy 181 AASYFIRDSTDSTLRLLHHIQIASTAIIKVTETRGPUCSYDNLDVSVLVQSPENPKIQL 240
 DB 168 ASSYFVDRTGTMRRJHEIQ1STGA KVTETRGPUCGSNDLDSVSVLQSTESTKLHL 227
 Qy 241 QGLQVILPDYLQERFVQALSYIACNSEGFFICKENDCNCCHGKPKFECNCPSMDIQAME 300
 DB 228 QGLQIQTQPLQEKEVQSVQCSQRCQACEPQCNCPITDQIME 287
 Qy 301 ENLLRITETKAYNSDFEESDEFKFLMKLPMYFLNTSTIMHLMTMDNSNFQRRYEQLEN 360
 DB 288 FTLANWAKANTEAYDLENSDEFKSFMKLPNSHFTLIGTSIHONGNDWDLQSRYKLQSQ 347
 Qy 361 SMKQFLKAQIVHKLFSLSKRKHQPLISLSPROFTSYULTRIOSFLYCNENGLLGSFS 420
 DB 348 ATERQRQKIORTARKLFLGLSVRCHRNPHOLPRETTIQWMLARYOSLYNCENGFWGTFL 407
 Qy 421 EETHSCSTCPNDQVVCTAFLPCTVGDAACLTCAPDNTRCTGTGMLLSQGLCKPVAE 480
 DB 408 ESQRSCVCHESSTLQRPICPIIGNNSCAMSLANISLGSCNCNGKYKLVRGRCEPQNVD 467
 Qy 481 S-TDHYIGFETDL--QDLEMKYLQKTDRTBRIEVHAIFISNDMRUWSFDPWSRKMLLT 536
 DB 468 SERSEQFISPTEDLDQDLEBLKYLQKMDSRLYVHTTFISNETRUDFFDPRWRKMSLT 527
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 DB 528 LKSNKVKSSLVHMIGMSRMCQNSLSDPMFFYYVNPFGSGSHSEGWMNPFGEGFSYPRW 587
 Qy 597 ERTKLDPLOCYNTLGNKWKTEFETYIYLRSRIKSNGPNENSYYPEPLEFIDPSR 656
 DB 588 EKIRLO-NSQCYNWLLGARWKCFEFETVHILYLSRTRL--PLRNETGGPVDLSDPSK 644
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